## AMENDMENT

***In the Claims:***

The following listing of claims will replace all prior versions, and listings, of claims in the application. Please cancel claims 33 and 34 (claims 1-3 and 8-12 and 30 were previously canceled). Currently amended claims (*i.e.*, claims 13, 15, 21, 25 and 35) are shown with additions underlined and deletions in ~~strikethrough text~~. No new matter is added by this amendment.

1.-3. (Canceled)

4. (Previously presented) The method of claim 25, wherein the mixture of molecules includes a mixture of isolated peptides.

5. (Previously presented) The method of claim 25, wherein the mixture of molecules includes molecules that are water soluble and have a molecular weight greater than 400.

6. (Previously presented) The method of claim 25, wherein the bioassay includes an electrospray process.

7. (Previously presented) The method of claim 25, wherein the bioassay includes a biochip-based process.

8. - 12. (Canceled)

13. (Currently amended) The method of claim 25~~12~~, wherein the determining whether the test centroid is within a predetermined distance includes one of: determining that the bioassay process is functioning properly when the test centroid is within or is equal to the predetermined distance from the control centroid, and determining that the bioassay process is not functioning properly when the test centroid is beyond the predetermined distance from the control centroid.

14. (Previously presented) The method of claim 25, wherein each of the features is a mass-to-charge ratio.

15. (Currently amended) A method of evaluating the results from a bioassay process, the method comprising:

preparing a mixture of molecules;

dividing the mixture of molecules into a plurality of aliquots;

preserving the plurality of aliquots;

retrieving a first aliquot, the first aliquot being a control aliquot;

obtaining data from the control aliquot using the bioassay process, the data including values for n features, which collectively define a control centroid in an n-dimenstional space;

subsequently retrieving a second aliquot, the second aliquot being a test aliquot;

obtaining data from the test aliquot using the bioassay process, the data including values for the n features, which collectively define a test centroid in the n-dimensional space; and

determining whether the displacement in the n-dimensional space of the test centroid exceeds a predetermined distance from the control centroid as an indication of whether the bioassay has generated unreliable results.

16. (Previously presented) The method of claim 15, wherein the obtaining data from the control aliquot using the bioassay process includes using an electrospray process.

17. (Previously presented) The method of claim 15, wherein the obtaining data from the control aliquot using the bioassay process includes using a biochip.

18. (Previously presented) The method of claim 15, wherein the obtaining data from the control aliquot includes:

selecting a subset of n features from a plurality of features associated with the control aliquot.

19. (Previously presented) The method of claim 15, wherein each feature is a mass-to-charge ratio and the value of each feature is a magnitude.

20. (Previously presented) The method of claim 15, wherein the retrieving a first aliquot includes retrieving two or more aliquots.

21. (Currently amended) A method of evaluating the results from a bioassay process, comprising:

retrieving a test aliquot of a preserved molecular mixture;

analyzing data from the test aliquot using a bioassay process;

comparing a test set of features of the test aliquot with a control set of features based on a control aliquot from the preserved molecular mixture, the control set of features defining a control centroid in an n-dimensional space, the test set of features defining a test centroid in the

n-dimensional space, the test set of features of the retrieved mixture being the same as the control set of features; and

determining whether the position of the test centroid is greater than a predetermined displacement from the control centroid as an indication of whether the bioassay has generated unreliable results.

22. (Previously presented) The method of claim 21, wherein said features are mass-to-charge ratios and wherein said comparing includes comparing magnitudes of each of the test set of mass-to-charge ratios with the magnitudes of the control set of mass-to-charge ratios.

23. (Previously presented) The method of claim 21, wherein the analyzing data from the test aliquot using a bioassay process includes analyzing data from the test aliquot using an electrospray process.

24. (Previously presented) The method of claim 21, wherein the analyzing data from the test aliquot using a bioassay process includes analyzing data from the test aliquot using a biochip.

25. (Currently amended) A method for evaluating the results from a bioassay that generates spectral data, comprising:

providing a location in an n-dimensional space of a control centroid associated with control spectral data generated from a first aliquot of a prepared mixture of molecules;

generating test spectral data from a second aliquot of the mixture;

computing a location in the n-dimensional space of a test centroid associated with the test spectral data;

comparing the test centroid to the control centroid to determine the displacement in n-dimensional space of the test centroid from the control centroid; and

determining whether the test centroid is greater than a predetermined displacement from the control centroid as an indication of whether the bioassay has generated unreliable results.

26. (Previously presented) The method of claim 25, wherein the mixture of molecules is a biological sample.

27. (Previously presented) The method of claim 25, wherein the spectral data are generated by a mass spectrometer.

28. (Canceled)

29. (Previously presented) The method of claim 25, further comprising repeating the generating test spectral data and computing a location for multiple aliquots of the mixture of molecules over time to monitor performance of the bioassay.

30. (Canceled)

31. (Previously presented) The method of claim 21, wherein the predetermined displacement is two standard deviations.

32. (Previously presented) The method of claim 25, wherein the mixture of molecules is selected from the group consisting of naturally-occurring and non-naturally-occurring molecules.

33-34. (Canceled)

35. (Currently amended) A method for evaluating the results from a bioassay that generates spectral data, comprising:

providing a location in an n-dimensional space of a control centroid associated with control spectral data generated from a first aliquot of a prepared mixture of molecules;

providing a location in an n-dimensional space of a test centroid associated with test spectral data generated from a second aliquot of the prepared mixture of molecules;

comparing the test centroid to the control centroid to determine the displacement in n-dimensional space of the test centroid from the control centroid; and

determining whether the displacement in n-dimensional space of the test centroid exceeds a predetermined distance from the control centroid, wherein the determining whether the test centroid is within a predetermined distance includes one of: determining that the bioassay process is functioning properly when the test centroid is within or is equal to the predetermined distance from the control centroid, and determining that the bioassay process is not functioning properly when the test centroid is beyond the predetermined distance from the control centroid.